

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Mixson, James A

(ii) TITLE OF INVENTION: CARRIER:NUCLEIC ACIDS COMPLEXES CONTAINING
NUCLEIC ACIDS ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN
GENE THERAPY

(iii) NUMBER OF SEQUENCES: 43

(iv) CORRESPONDENCE ADDRESS:

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- (C) CITY: Wilmington
- (D) STATE: Delaware
- (E) COUNTRY: U.S.A.
- (F) ZIP: 19899

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk (provided in parent application)
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: Not yet assigned
- (B) FILING DATE:
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/985,526
- (B) FILING DATE: 5-DEC-1997

(viii) ATTORNEY/AGENT INFORMATION:

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(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Thr Glu Glu Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro
1 5 10 15

Leu Cys Tyr His Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr
20 25 30

Val Asp Ser Cys Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys
35 40 45

Lys Lys Val Ser Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro
50 55 60

Asp Gly Glu Cys Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp
65 70 75 80

Gly Trp Ser Pro Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly
85 90 95

Asn Gly Ile Gln Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg
100 105 110

Cys Glu Gly Ser Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys
115 120 125

Asp Lys Arg Phe Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp
130 135 140

Ser Ser Cys Ser Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Thr
145 150 155 160

Asn Leu Cys Ser Pro Ser Pro Gln Met Asn Gly Lys Pro Cys Glu Gly
165 170 175

Arg Glu Ala Glu Thr Lys Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn

180 185 190

Gly Gly Trp Gly Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys
195 200 205

Gly Gly Gly Val Gln Lys Arg Ser Arg Leu
210 215

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGACTGAAG AGAACAAAGA GTTGGCCAAT GAGCTGAGGC GGCCTCCCCT
ATGCTATCAC 60

AACGGAGTTC AGTACAGAAA TAACGAGGAA TGGACTGTTG ATAGCTGCAC
TGAGTGTAC 120

TGTCAGAACT CAGTTACCAT CTGCAAAAAG GTGTCCTGCC CCATCATGCC
CTGCTCCAAT 180

GCCACAGTTC CTGATGGAGA ATGCTGTCCT CGCTGTTGGC CCAGCGACTC
TGCGGACGAT 240

GGCTGGTCTC CATGGTCCGA GTGGACCTCC TGTTCTACGA GCTGTGGCAA
TGGAATTCAG 300

CAGCGCGGCC GCTCCTGCGA TAGCCTCAAC AACCGATGTG AGGGCTCCTC
GGTCCAGACA 360

CGGACCTGCC ACATTCAGGA GTGTGACAAA AGATTAAAC AGGATGGTGG
CTGGAGCCAC 420

TGGTCCCCGT GGTCATCTTG TTCTGTGACA TGTGGTGATG GTGTGATCAC
AAGGATCCGG 480

CTCTGCAACT CTCCCAGCCC CCAGATGAAT GGGAAACCCT GTGAAGGCGA
AGCGCGGGAG 540

ACCAAAGCCT GCAAGAAAGA CGCCTGCCCC ATCAATGGAG GCTGGGGTCC
TTGGTCACCA 600

TGGGACATCT GTTCTGTCAC CTGTGGAGGA GGGGTACAGA AACGTAGTCG
TCTCTAA 656

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 441 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Thr Glu Glu Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro
1 5 10 15

Leu Cys Tyr His Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr
20 25 30

Asp Val Ser Cys Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys
35 40 45

Lys Lys Val Ser Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro
50 55 60

Asp Gly Glu Cys Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp
65 70 75 80

Trp Gly Ser Pro Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly
85 90 95

Gly Asn Ile Gln Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg
100 105 110

Cys Glu Gly Ser Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys
115 120 125

Asp Lys Arg Phe Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp
130 135 140

Ser Ser Cys Ser Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Thr
145 150 155 160

Leu Cys Asn Ser Pro Ser Pro Gln Met Asn Gly Lys Pro Cys Glu Gly
165 170 175

Glu Ala Arg Glu Thr Lys Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn
180 185 190

Gly Gly Trp Gly Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys
195 200 205

Gly Gly Gly Val Gln Lys Arg Ser Arg Leu Cys Val Asp Ser Arg Met
210 215 220

Thr Glu Glu Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu
225 230 235 240

Cys Tyr His Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val
245 250 255

Asp Ser Cys Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys
260 265 270

Lys Val Ser Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp
275 280 285

Gly Glu Cys Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly
290 295 300

Trp Ser Pro Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn
305 310 315 320

Gly Ile Gln Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys
325 330 335

Glu Gly Ser Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp
340 345 350

Lys Arg Phe Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser
355 360 365

Ser Cys Ser Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Thr Leu
370 375 380

Cys Asn Ser Pro Ser Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu
385 390 395 400

Ala Arg Glu Thr Lys Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Gly
405 410 415

Gly Trp Gly Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly
420 425 430

Gly Gly Val Gln Lys Arg Ser Arg Leu
435 440

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGACTGAAG AGAACAAAGA GTTGGCCAAT GAGCTGAGGC GGCCTCCCCT
ATGCTATCAC 60

AACGGAGTTC AGTACAGAAA TAACGAGGAA TGGACTGTTG ATAGCTGCAC
TGAGTGTCAC 120

TGTCAGAACT CAGTTACCAT CTGCAAAAAG GTGTCCTGCC CCATCATGCC
CTGCTCCAAT 180

GCCACAGTTC CTGATGGAGA ATGCTGTCCT CGCTGTTGGC CCAGCGACTC
TGCGGACGAT 240

GGCTGGTCTC CATGGTCCGA GTGGACCTCC TGTTCTACGA GCTGTGGCAA
TGGAATTCAG 300

CAGCGCGGCC GCTCCTGCGA TAGCCTCAAC AACCGATGTG AGGGCTCCTC

GGTCCAGACA 360

CGGACCTGCC ACATTCAGGA GTGTGACAAA AGATTTAAAC AGGATGGTGG
CTGGAGCCAC 420

TGGTCCCCGT GGTCATCTTG TTCTGTGACA TGTGGTGATG GTGTGATCAC
AAGGATCCGG 480

CTCTGCAACT CTCCCAGCCC CCAGATGAAT GGGAAACCCT GTGAAGGCGA
AGCGCGGGAG 540

ACCAAAGCCT GCAAGAAAGA CGCCTGCCCC ATCAATGGAG GCTGGGGTCC
TTGGTCACCA 600

TGGGACATCT GTTCTGTCAC CTGTGGAGGA GGGGTACAGA AACGTAGTCG
TCTCTGCGTC 660

GACTCTAGAA TGACTIONGAAGA GAACAAAGAG TTGGCCAATG AGCTGAGGCG
GCCTCCCCTA 720

TGCTATCACA ACGGAGTTCA GTACAGAAAT AACGAGGAAT GGACTGTTGA
TAGCTGCACT 780

GAGTGTCACT GTCAGAACTC AGTTACCATC TGCAAAAAGG TGTCCTGCCC
CATCATGCCC 840

TGCTCCAATG CCACAGTTCC TGATGGAGAA TGCTGTCCTC GCTGTTGGCC
CAGCGACTCT 900

GCGGACGATG GCTGGTCTCC ATGGTCCGAG TGGACCTCCT GTTCTACGAG
CTGTGGCAAT 960

GGAATTCAGC AGCGCGGCCG CTCCTGCGAT AGCCTCAACA ACCGATGTGA
GGGCTCCTCG 1020

GTCCAGACAC GGACCTGCCA CATTGAGGAG TGTGACAAAA GATTTAAACA
GGATGGTGGC 1080

TGGAGCCACT GGTCCCCGTG GTCATCTTGT TCTGTGACAT GTGGTGATGG
TGTGATCACA 1140

AGGATCCGGC TCTGCAACTC TCCCAGCCCC CAGATGAATG GGAAACCCTG
TGAAGGCGAA 1200

GCGCGGGAGA CCAAAGCCTG CAAGAAAGAC GCCTGCCCCA TCAATGGAGG

CTGGGGTCCT 1260

TGGTCACCAT GGGACATCTG TTCTGTCACC TGTGGAGGAG GGGTACAGAA
ACGTAGTCGT 1320

CTCTAA

1326

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Tyr Ile Gly Ser Arg

1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTCGACATGT ATATTGGTTC TCGTTAAGTC GAC

33

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

[illegible]

Ser Tyr Ile Gly Ser Arg Gly Lys Ser
20 25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

GTCGACATGT ATATTGGTTC TCGTGTA AAA GTTATATTGG TTCTCGTGGT
AAAAGTTATA 60

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

Met Leu Tyr Lys Lys Ile Ile Lys Lys Leu Leu Glu Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTCGACATGC TTTATAAGAA GATCATCAAG AAGCTTCTTG AGAGTTAAGT CGAC
54

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Leu Tyr Lys Lys Ile Ile Lys Lys Leu Leu Glu Ser Gly Lys Ser
1 5 10 15

Leu Tyr Lys Lys Ile Ile Lys Lys Leu Leu Glu Ser Gly Lys Ser Leu
20 25 30

Tyr Lys Lys Ile Ile Lys Lys Leu Leu Glu Ser Gly Lys Ser
35 40 45

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTCGACATGC TTTATAAGAA GATCATCAAG AAGCTTCTTG AGAGTGGTAA
AAGTCTTTAT 60

AAGAAGATCA TCAAGAAGCT TCTTGAGAGT GGTAAAAGTC TTTATAAGAA
GATCATCAAG 120

AAGCTTCTTG AGAGTGGTAA AAGTTAAGTC GAC 153

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Phe Cys Tyr Trp Lys Val Cys Trp
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTCGACATGT TCTGTTATTG GAAGGTTTGT TGGTAAGTCG AC

42

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Phe Cys Tyr Trp Lys Val Cys Trp Gly Lys Ser Phe Cys Tyr Trp
1 5 10 15

Lys Val Cys Trp Gly Lys Ser Phe Cys Tyr Trp Lys Val Cys Trp Gly
20 25 30

Lys Ser

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTCGACATGT TCTGTTATTG GAAGGTTTGT TGGGGTAAAA GTTTCTGTTA
TTGGAAGGT 60

TGTTGGGGTA AAAGTTTCTG TTATTGGAAG GTTTGTTGGG GTAAAAGTTA
AGTCGAC 117

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Gly Arg Gly Asp

1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTCGACATGG GTCGTGGTGA TTAAGTCGAC

30

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Gly Arg Gly Asp Gly Lys Ser Gly Arg Gly Asp Gly Lys Ser Gly

1 5 10 15

Arg Gly Asp Gly Lys Ser
20

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GTCGACATGG GTCGTGGTGA TGGTAAAAGT GGTCGTGGTG ATGGTAAAAG
TGGTCGTGGT 60

GATGGTAAAA GTTAAGTCGA C 81

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Val Tyr Leu Ser Glu Cys Lys Thr Gly Ile Gly Asn Gly Tyr Arg
1 5 10 15

Gly Thr Met Ser Arg Thr Lys Ser Gly Val Ala Cys Gln Lys Trp Gly
20 25 30

Ala Thr Phe Pro His Val Pro Asn Tyr Ser Pro Ser Thr His Pro Asn
35 40 45

Glu Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Glu Gln

50 55 60
 Gly Pro Trp Cys Tyr Thr Thr Asp Pro Asp Lys Arg Tyr Asp Tyr Cys
 65 70 75 80
 Asn Ile Pro Glu Cys Glu Glu Glu Cys Met Tyr Cys Ser Gly Glu Lys
 85 90 95
 Tyr Glu Gly Lys Ile Ser Lys Thr Met Ser Gly Lys Asp Cys Gln Ala
 100 105 110
 Trp Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ala Lys Phe
 115 120 125
 Pro Ser Lys Asn Leu Lys Met Asn Tyr Cys His Asn Pro Asp Gly Glu
 130 135 140
 Pro Arg Pro Trp Cys Phe Thr Thr Asp Pro Thr Lys Arg Trp Glu Tyr
 145 150 155 160
 Cys Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Pro Pro Ser Pro Thr
 165 170 175
 Tyr Gln Cys Leu Lys Gly Arg Gly Glu Asn Tyr Arg Gly Thr Val Ser
 180 185 190
 Val Thr Val Ser Gly Lys Thr Cys Gln Arg Trp Ser Glu Gln Thr Pro
 195 200 205
 His Arg
 210

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GTCTGACATGG TGTATCTGTC AGAATGTAAG ACCGGCATCG GCAACGGCTA
CAGAGGAACC 60

ATGTCCAGGA CAAAGAGTGG TGTTGCCTGT CAAAAGTGGG GTGCCACGTT
CCCCACGTA 120

CCCAACTACT CTCCCAGTAC ACATCCCAAT GAGGGACTAG AAGAGAACTA
CTGTAGGAAC 180

CCAGACAATG ATGAACAAGG GCCTTGGTGC TAACTACAG ATCCGGACAA
GAGATATGAC 240

TACTGCAACA TTCCTGAATG TGAAGAGGAA TGCATGTACT GCAGTGGAGA
AAAGTATGAG 300

GGCAAAATCT CCAAGACCAT GTCTGGACTT GACTGCCAGG CCTGGGATTC
TCAGAGCCCA 360

CATGCTCATG GATACATCCC TGCCAAATTT CCAAGCAAGA ACCTGAAGAT
GAATTATTGC 420

CACAACCCTG ACGGGGAGCC AAGGCCCTGG TGCTTCACAA CAGACCCAC
CAAACGCTGG 480

GAATACTGTG ACATCCCCCG CTGCACAACA CCCCCGCCCC CACCCAGCCC
AACCTACCA 540

TGTCTGAAAG GAAGAGGTGA AAATTACCGA GGGACCGTGT CTGTCACCGT
GTCTGGGAAA 600

ACCTGTCAGC GCTGGAGTGA GCAAACCCCT CATAGGTGAG TCGAC

644

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

1003669-17901

Met Val Tyr Leu Ser Glu Cys Lys Thr Gly Ile Gly Asn Gly Tyr Arg
1 5 10 15

Gly Thr Met Ser Arg Thr Lys Ser Gly Val Ala Cys Gln Lys Trp Gly
20 25 30

Ala Thr Phe Pro His Val Pro Asn Tyr Ser Pro Ser Thr His Pro Asn
35 40 45

Glu Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Glu Gln
50 55 60

Gly Pro Trp Cys Tyr Thr Thr Asp Pro Asp Lys Arg Tyr Asp Tyr Cys
65 70 75 80

Asn Ile Pro Glu Cys Glu Glu Glu Cys Met Tyr Cys Ser Gly Glu Lys
85 90 95

Tyr Glu Gly Lys Ile Ser Lys Thr Met Ser Gly Lys Asp Cys Gln Ala
100 105 110

Trp Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ala Lys Phe
115 120 125

Pro Ser Lys Asn Leu Lys Met Asn Tyr Cys His Asn Pro Asp Gly Glu
130 135 140

Pro Arg Pro Trp Cys Phe Thr Thr Asp Pro Thr Lys Arg Trp Glu Tyr
145 150 155 160

Cys Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Pro Ser Pro Thr
165 170 175

Tyr Gln Cys Leu Lys Gly Arg Gly Glu Asn Tyr Arg Gly Thr Val Ser
180 185 190

Val Thr Val Ser Gly Lys Thr Cys Gln Arg Trp Ser Glu Gln Thr Pro
195 200 205

His Arg Gly Lys Ser Met Val Tyr Leu Ser Glu Cys Lys Thr Gly Ile
210 215 220

Gly Asn Gly Tyr Arg Gly Thr Met Ser Arg Thr Lys Ser Gly Val Ala
225 230 235 240

Cys Gln Lys Trp Gly Ala Thr Phe Pro His Val Pro Asn Tyr Ser Pro
245 250 255

Ser Thr His Pro Asn Glu Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro
260 265 270

Asp Asn Asp Glu Gln Gly Pro Trp Cys Tyr Thr Thr Asp Pro Asp Lys
275 280 285

Arg Tyr Asp Tyr Cys Asn Ile Pro Glu Cys Glu Glu Glu Cys Met Tyr
290 295 300

Cys Ser Gly Glu Lys Tyr Glu Gly Lys Ile Ser Lys Thr Met Ser Gly
305 310 315 320

Lys Asp Cys Gln Ala Trp Asp Ser Gln Ser Pro His Ala His Gly Tyr
325 330 335

Ile Pro Ala Lys Phe Pro Ser Lys Asn Leu Lys Met Asn Tyr Cys His
340 345 350

Asn Pro Asp Gly Glu Pro Arg Pro Trp Cys Phe Thr Thr Asp Pro Thr
355 360 365

Lys Arg Trp Glu Tyr Cys Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro
370 375 380

Pro Pro Ser Pro Thr Tyr Gln Cys Leu Lys Gly Arg Gly Glu Asn Tyr
385 390 395 400

Arg Gly Thr Val Ser Val Thr Val Ser Gly Lys Thr Cys Gln Arg Trp
405 410 415

Ser Glu Gln Thr Pro His Arg
420

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTCGACATGG TGTATCTGTC AGAATGTAAG ACCGGCATCG GCAACGGCTA
CAGAGGAACC 60

ATGTCCAGGA CAAAGAGTGG TGTTGCCTGT CAAAAGTGGG GTGCCACGTT
CCCCACGTA 120

CCCAACTACT CTCCAGTAC ACATCCCAAT GAGGGACTAG AAGAGAACTA
CTGTAGGAAC 180

CCAGACAATG ATGAACAAGG GCCTTGGTGC TACTACTACAG ATCCGGACAA
GAGATATGAC 240

TACTGCAACA TTCCTGAATG TGAAGAGGAA TGCATGTACT GCAGTGGAGA
AAAGTATGAG 300

GGCAAAATCT CCAAGACCAT GTCTGGACTT GACTGCCAGG CCTGGGATTC
TCAGAGCCCA 360

CATGCTCATG GATACATCCC TGCCAAATTT CCAAGCAAGA ACCTGAAGAT
GAATTATTGC 420

CACAACCCTG ACGGGGAGCC AAGGCCCTGG TGCTTCACAA CAGACCCAC
CAAACGCTGG 480

GAATACTGTG ACATCCCCCG CTGCACAACA CCCCCGCCCC CACCCAGCCC
AACCTACCAA 540

TGTCTGAAAG GAAGAGGTGA AAATTACCGA GGGACCGTGT CTGTCACCGT
GTCTGGGAAA 600

ACCTGTCAGC GCTGGAGTGA GCAAACCCCT CATAGGGGTA AAAGTATGGT
GTATCTGTCA 660

GAATGTAAGA CCGGCATCGG CAACGGCTAC AGAGGAACCA TGTCCAGGAC
AAAGAGTGGT 720

GTTGCCTGTC AAAAGTGGGG TGCCACGTTC CCCCACGTAC CCAACTACTC
TCCCAGTACA 780

CATCCCAATG AGGGACTAGA AGAGAACTAC TGTAGGAACC CAGACAATGA
TGAACAAGGG 840

CCTTGGTGCT ACACTACAGA TCCGGACAAG AGATATGACT ACTGCAACAT
TCCTGAATGT 900

GAAGAGGAAT GCATGTACTG CAGTGGAGAA AAGTATGAGG GCAAAATCTC
CAAGACCATG 960

TCTGGACTTG ACTGCCAGGC CTGGGATTCT CAGAGCCCAC ATGCTCATGG
ATACATCCCT 1020

GCCAAATTTC CAAGCAAGAA CCTGAAGATG AATTATTGCC ACAACCCTGA
CGGGGAGCCA 1080

AGGCCCTGGT GCTTCACAAC AGACCCCACC AAACGCTGGG AATACTGTGA
CATCCCCCGC 1140

TGCACAACAC CCCC GCCCCC ACCCAGCCCA ACCTACCAAT GTCTGAAAGG
AAGAGGTGAA 1200

AATTACCGAG GGACCGTGTC TGTCACCGTG TCTGGGAAAA CCTGTCAGCG
CTGGAGTGAG 1260

CAAACCCCTC ATAGGTGAGT CGAC 1284

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Leu Pro Ile Cys Pro Gly Gly Ala Ala Arg Cys Gln Val Thr Leu
1 5 10 15

Arg Glu Leu Phe Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn
20 25 30

Leu Ser Ser Glu Met Phe Ser Glu Phe Glu Lys Arg Tyr Thr His Gly
35 40 45

Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu
50 55 60

Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
65 70 75 80

Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu
85 90 95

Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Gln Ala
100 105 110

Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr Lys
115 120 125

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTCGACATGT TGCCCATCTG TCCCGGCGGG GCTGCCCCGAT GCCAGGTGAC
CCTTCGAGAC 60

CTGTTTGACC GCGCCGTCGT CCTGTCCCAC TACATCCATA ACCTCTCCTC
AGAAATGTTC 120

AGCGAATTCG ATAAACGGTA TACCCATGGC CGGGGGTTCA TTACCAAGGC
CATCAACAGC 180

TGCCACACTT CTTCCCTTGC CACCCCCGAA GACAAGGAGC AAGCCCAACA
GATGAATCAA 240

AAAGACTTTC TGAGCCTGAT AGTCAGCATA TTGCGATCCT GGAATGAGCC
TCTGTATCAT 300

CTGGTCACGG AAGTACGTGG TATGCAAGAA GCCCCGGAGG CTATCCTATC

CAAAGCTGTA 360

GAGATTGAGG AGCAAACCAA ATAAGTCGAC

390

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Leu Pro Ile Cys Pro Gly Gly Ala Ala Arg Cys Gln Val Thr Leu
1 5 10 15

Arg Glu Leu Phe Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn
20 25 30

Leu Ser Ser Glu Met Phe Ser Glu Phe Glu Lys Arg Tyr Thr His Gly
35 40 45

Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu
50 55 60

Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
65 70 75 80

Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu
85 90 95

Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Gln Ala
100 105 110

Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr Lys Gly Lys Ser
115 120 125

Met Leu Pro Ile Cys Pro Gly Gly Ala Ala Arg Cys Gln Val Thr Leu
130 135 140

Arg Glu Leu Phe Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn

145 150 155 160
 Leu Ser Ser Glu Met Phe Ser Glu Phe Glu Lys Arg Tyr Thr His Gly
 165 170 175
 Arg Gly Phe Ile Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu
 180 185 190
 Ala Thr Pro Glu Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp
 195 200 205
 Phe Leu Ser Leu Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu
 210 215 220
 Tyr His Leu Val Thr Glu Val Arg Gly Met Gln Glu Ala Pro Gln Ala
 225 230 235 240
 Ile Leu Ser Lys Ala Val Glu Ile Glu Glu Gln Thr Lys
 245 250

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTCGACATGT TGCCCATCTG TCCCGGCGGG GCTGCCCGAT GCCAGGTGAC
 CCTTCGAGAC 60
 CTGTTTGACC GCGCCGTCGT CCTGTCCAC TACATCCATA ACCTCTCCTC
 AGAAATGTTC 120
 AGCGAATTCG ATAAACGGTA TACCCATGGC CGGGGGTTCA TTACCAAGGC
 CATCAACAGC 180
 TGCCACACTT CTTCCCTTGC CACCCCCGAA GACAAGGAGC AAGCCCAACA
 GATGAATCAA 240

[illegible]

AAAAGAAGTG 120

GTACCCTGTA GACAAGACAG TGGACACCTC CTCCCCATTA A

161

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Leu Arg Arg Pro Pro Leu Cys Tyr His Asn Gly Val Gln Tyr Arg
1 5 10 15

Asn Asn Glu Glu Trp Thr Val Asp Ser Gly Lys Ser Ser Pro Trp Ser
20 25 30

Ser Cys Ser Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Gly Lys
35 40 45

Ser Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly Gly Gly Val
50 55 60

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGCTGAGGC GGCCTCCCCT ATGCTATCAC AACGGAGTTC AGTACAGAAA
TAACGGTAAA 60

AGATCCCCGT GGTCATCTTG TTCTGTGACA TGTGGTGATG GTGTGATGGT
AAAAGAAGTG 120

GTACCCTGTA GACAAGACAG TGGACACCTC CTCCCCATTA TATTGGTTCT
CGTGGTAAAA 180

GATAA 185

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TAGGTCTAGA ATGACTGAAG AGAACAAAGA G 31

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGGTCTAGA TTAGAGACGA CTACGTTTCT G 31

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 805 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Glu Ser Lys Ala Leu Leu Ala Val Ala Leu Trp Phe Cys Val Glu
1 5 10 15

Thr Arg Ala Ala Ser Val Gly Leu Pro Gly Asp Phe Leu His Pro Pro
20 25 30

Lys Leu Ser Thr Gln Lys Asp Ile Leu Thr Ile Leu Ala Asn Thr Thr
35 40 45

Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro
50 55 60

Asn Ala Gln Arg Asp Ser Glu Glu Arg Val Leu Val Thr Glu Cys Gly
65 70 75 80

Gly Gly Asp Ser Ile Phe Cys Lys Thr Leu Thr Ile Pro Arg Val Val
85 90 95

Gly Asn Asp Thr Gly Ala Tyr Lys Cys Ser Tyr Arg Asp Val Asp Ile
100 105 110

Ala Ser Thr Val Tyr Val Tyr Val Arg Asp Tyr Arg Ser Pro Phe Ile
115 120 125

Ala Ser Val Ser Asp Gln His Gly Ile Val Tyr Ile Thr Glu Asn Lys
130 135 140

Asn Lys Thr Val Val Ile Pro Cys Arg Gly Ser Ile Ser Asn Leu Asn
145 150 155 160

Val Ser Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly
165 170 175

Asn Arg Ile Ser Trp Asp Ser Glu Ile Gly Phe Thr Leu Pro Ser Tyr
180 185 190

Met Ile Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp

1003669.12901

195 200 205
Glu Thr Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg
210 215 220
Ile Tyr Asp Val Ile Leu Ser Pro Pro His Glu Ile Glu Leu Ser Ala
225 230 235 240
Gly Glu Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val
245 250 255
Gly Leu Asp Phe Thr Trp His Ser Pro Pro Ser Lys Ser His His Lys
260 265 270
Lys Ile Val Asn Arg Asp Val Lys Pro Phe Pro Gly Thr Val Ala Lys
275 280 285
Met Phe Lys Ser Thr Leu Thr Ile Glu Ser Val Thr Lys Ser Asp Gln
290 295 300
Gly Glu Tyr Thr Cys Val Ala Ser Ser Gly Arg Met Ile Lys Arg Asn
305 310 315 320
Arg Thr Phe Val Arg Val His Thr Lys Pro Phe Ile Ala Phe Gly Ser
325 330 335
Gly Met Lys Ser Leu Val Glu Ala Thr Val Gly Ser Gln Val Arg Ile
340 345 350
Pro Val Lys Tyr Leu Ser Tyr Pro Ala Pro Asp Ile Lys Trp Tyr Arg
355 360 365
Asn Gly Arg Pro Ile Glu Ser Asn Tyr Thr Met Ile Val Gly Asp Glu
370 375 380
Leu Thr Ile Met Glu Val Thr Glu Arg Asp Ala Gly Asn Tyr Thr Val
385 390 395 400
Ile Leu Thr Asn Pro Ile Ser Met Glu Lys Gln Ser His Met Val Ser
405 410 415
Leu Val Val Asn Val Pro Pro Gln Ile Gly Glu Lys Ala Leu Ile Ser
420 425 430

Pro Met Asp Ser Tyr Gly Tyr Gly Thr Met Gln Thr Leu Thr Cys Thr
435 440 445

Val Tyr Ala Asn Pro Pro Leu His His Ile Gln Trp Tyr Trp Gln Leu
450 455 460

Glu Glu Ala Cys Ser Tyr Arg Pro Gly Gln Thr Ser Pro Tyr Ala Cys
465 470 475 480

Lys Glu Trp Arg His Val Glu Asp Phe Gln Gly Gly Asn Lys Ile Glu
485 490 495

Val Thr Lys Asn Gln Tyr Ala Leu Ile Glu Gly Lys Asn Lys Thr Val
500 505 510

Ser Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr Lys Cys
515 520 525

Glu Ala Ile Asn Lys Ala Gly Arg Gly Glu Arg Val Ile Ser Phe His
530 535 540

Val Ile Arg Gly Pro Glu Ile Thr Val Gln Pro Ala Ala Gln Pro Thr
545 550 555 560

Glu Gln Glu Ser Val Ser Leu Leu Cys Thr Ala Asp Arg Asn Thr Phe
565 570 575

Glu Asn Leu Thr Trp Tyr Lys Leu Gly Ser Gln Ala Thr Ser Val His
580 585 590

Met Gly Glu Ser Leu Thr Pro Val Cys Lys Asn Leu Asp Ala Leu Trp
595 600 605

Lys Leu Asn Gly Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile
610 615 620

Val Ala Phe Gln Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys
625 630 635 640

Ser Ala Gln Asp Lys Lys Thr Lys Lys Arg His Cys Leu Val Lys Gln
645 650 655

Leu Ile Ile Leu Glu Arg Met Ala Pro Met Ile Thr Gly Asn Leu Glu
660 665 670

Asn Gln Thr Thr Thr Ile Gly Glu Thr Ile Glu Val Thr Cys Pro Ala
675 680 685

Ser Gly Asn Pro Thr Pro His Ile Thr Trp Phe Lys Asp Asn Glu Thr
690 695 700

Leu Val Glu Asp Ser Gly Ile Val Leu Arg Asp Gly Asn Arg Asn Leu
705 710 715 720

Thr Ile Arg Arg Val Arg Lys Glu Asp Gly Gly Leu Tyr Thr Cys Gln
725 730 735

Ala Cys Asn Val Leu Gly Cys Ala Arg Ala Glu Thr Leu Phe Ile Ile
740 745 750

Glu Gly Ala Gln Glu Lys Thr Asn Leu Glu Val Ile Ile Leu Val Gly
755 760 765

Thr Ala Val Ile Ala Met Phe Phe Trp Leu Leu Leu Val Ile Leu Val
770 775 780

Arg Thr Val Lys Arg Ala Asn Glu Gly Glu Leu Lys Thr Gly Tyr Leu
785 790 795 800

Ser Ile Val Met Asp
805

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGACGTCATG GAGAGCAAGG CGCTGCTAGC TGTCGCTCTG TGGTTCTGCG
TGGAGACCCG 60

AGCCGCCTCT GTGGGTTTGC CTGGCGATTT TCTCCATCCC CCCAAGCTCA
GCACACAGAA 120

AGACATACTG ACAATTTTGG CAAATACAAC CCTTCAGATT ACTTGCAGGG
GACAGCGGGA 180

CCTGGACTGG CTTTGGCCCA ATGCTCAGCG TGATTCTGAG GAAAGGGTAT
TGGTGACTGA 240

ATGCGGCGGT GGTGACAGTA TCTTCTGCAA AACACTCACC ATTCCCAGGG
TGGTTGAAA 300

TGATACTGGA GCCTACAAGT GCTCGTACCG GGACGTCGAC ATAGCCTCCA
CTGTTTATGT 360

CTATGTTCTGA GATTACAGAT CACCATTCAT CGCCTCTGTC AGTGACCAGC
ATGGCATCGT 420

GTACATCACC GAGAACAAGA ACAAACCTGT GGTGATCCCC TGCCGAGGGT
CGATTTCAAA 480

CCTCAATGTG TCTCTTTGCG CTAGGTATCC AGAAAAGAGA TTTGTTCCGG
ATGGAAACAG 540

AATTTCTTGG GACAGCGAGA TAGGCTTTAC TCTCCCCAGT TACATGATCA
GCTATGCCGG 600

CATGGTCTTC TGTGAGGCAA AGATCAATGA TGAAACCTAT CAGTCTATCA
TGTACATAGT 660

TGTGGTTGTA GGATATAGGA TTTATGATGT GATTCTGAGC CCCCCGCATG
AAATTGAGCT 720

ATCTGCCGGA GAAAAACTTG TCTTAAATTG TACAGCGAGA ACAGAGCTCA
ATGTGGGGCT 780

TGATTTACCC TGGCACTCTC CACCTTCAAA GTCTCATCAT AAGAAGATTG
TAAACCGGGA 840

TGTGAAACCC TTTCTGGGA CTGTGGCGAA GATGTTTTTG AGCACCTTGA
CAATAGAAAG 900

TGTGACCAAG AGTGACCAAG GGAATACAC CTGTGTAGCG TCCAGTGGAC
GGATGATCAA 960

GAGAAATAGA ACATTTGTCC GAGTTCACAC AAAGCCTTTT ATTGCTTTTCG
GTAGTGGGAT 1020

GAAATCTTTG GTGGAAGCCA CAGTGGGCAG TCAAGTCCGA ATCCCTGTGA
AGTATCTCAG 1080

TTACCCAGCT CCTGATATCA AATGGTACAG AAATGGAAGG CCCATTGAGT
CCAACTACAC 1140

AATGATTGTT GGCGATGAAC TCACCATCAT GGAAGTGAAT GAAAGAGATG
CAGGAAACTA 1200

CACGGTCATC CTCACCAACC CCATTTCAAT GGAGAAACAG AGCCACATGG
TCTCTCTGGT 1260

TGTGAATGTC CCACCCCAGA TCGGTGAGAA AGCCTTGATC TCGCCTATGG
ATTCCTACCA 1320

GTATGGGACC ATGCAGACAT TGACATGCAC AGTCTACGCC AACCTCCCC
TGCACCACAT 1380

CCAGTGGTAC TGGCAGCTAG AAGAAGCCTG CTCCTACAGA CCCGGCCAAA
CAAGCCCGTA 1440

TGCTTGTAAG GAATGGAGAC ACGTGGAGGA TTTCCAGGGG GGAAACAAGA
TCGAAGTCAC 1500

CAAAAACCAA TATGCCCTGA TTGAAGGAAA AAACAAAACCT GTAAGTACGC
TGGTCATCCA 1560

AGCTGCCAAC GTGTCAGCGT TGTACAAATG TGAAGCCATC AACAAAGCGG
GACGAGGAGA 1620

GAGGGTCATC TCCTTCCATG TGATCAGGGG TCCTGAAATT ACTGTGCAAC
CTGCTGCCCCA 1680

GCCAACTGAG CAGGAGAGTG TGTCCCTGTT GTGCACTGCA GACAGAAATA
CGTTTGAGAA 1740

CCTCACGTGG TACAAGCTTG GCTCACAGGC AACATCGGTC CACATGGGCG
AATCACTCAC 1800

ACCAGTTTGC AAGAACTTGG ATGCTCTTTG GAAACTGAAT GGCACCATGT
TTTCTAACAG 1860

CACAAATGAC ATCTTGATTG TGGCATTTC GAATGCCTCT CTGCAGGACC
AAGGCGACTA 1920

TGTTTGCTCT GCTCAAGATA AGAAGACCAA GAAAAGACAT TGCCTGGTCA
AACAGCTCAT 1980

CATCCTAGAG CGCATGGCAC CCATGATCAC CGGAAATCTG GAGAATCAGA
CAACAACCAT 2040

TGGCGAGACC ATTGAAGTGA CTTGCCCAGC ATCTGGAAAT CCTACCCAC
ACATTACATG 2100

GTTCAAAGAC AACGAGACCC TGGTAGAAGA TTCAGGCATT GTACTGAGAG
ATGGGAACCG 2160

GAACCTGACT ATCCGCAGGG TGAGGAAGGA GGATGGAGGC CTCTACACCT
GCCAGGCCTG 2220

CAATGTCCTT GGCTGTGCAA GAGCGGAGAC GCTCTTCATA ATAGAAGGTG
CCCAGGAAAA 2280

GACCAACTTG GAAGTCATTA TCCTCGTCGG CACTGCAGTG ATTGCCATGT
TCTTCTGGCT 2340

CCTTCTTGTC ATTCTCGTAC GGACCGTTAA GCGGGCCAAT GAAGGGGAAC
TGAAGACAGG 2400

CTACTTGTCT ATTGTCATGG ATTAAGACGT C 2431

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	His	Thr	His	Gln	Asp	Phe	Gln	Pro	Val	Leu	His	Leu	Val	Ala	Leu
1		5		10		15									

Asn Thr Pro Leu Ser Gly Gly Met Arg Gly Ile Arg Gly Ala Asp Phe
20 25 30

Gln Cys Phe Asn Asn Ala Arg Val Gly Leu Ser Gly Thr Phe Arg Ala
35 40 45

Phe Leu Ser Ser Arg Leu Gln Asp Leu Tyr Ser Ile Val Arg Arg Ala
50 55 60

Asp Arg Gly Ser Val Pro Ile Val Gln Asn Leu Arg Asp Glu Val Leu
65 70 75 80

Ser Pro Ser Trp Asp Ser Leu Phe Ser Gly Ser Gln Gly Gln Leu Gln
85 90 95

Pro Gly Ala Arg Ile Phe Ser Phe Asp Gly Arg Asp Val Leu Arg His
100 105 110

Pro Ala Trp Pro Gln Arg Ser Val Trp His Gly Ser Asp Pro Ser Gly
115 120 125

Arg Arg Leu Met Glu Ser Tyr Cys Glu Thr Trp Arg Thr Glu Thr Thr
130 135 140

Gly Ala Thr Gly Gln Ala Ser Ser Leu Leu Ser Gly Arg Leu Leu Glu
145 150 155 160

Gln Arg Ala Ala Ser Cys His Asp Ser Tyr Ile Val Leu Cys Ile Glu
165 170 175

Asn Ser Phe Met Thr Ser Phe Ser Arg
180 185

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AGACGTCATG CATACTCATC AGGACTTTCA GCCAGTGCTC CACCTGGTGG
CACTGAACAC 60

CCCCCTGTCT GGAGGCATGC GTGGTATCCG TGGAGCAGAT TTCCAGTGCT
TCCAGCAAGC 120

CCGAGCCGTG GGGCTGTCGG GCACCTTCCG GGCTTTCCTG TCCTCTAGGC
TGCAGGATCT 180

CTATAGCATC GTGCGCCGTG CTGACCGGGG GTCTGTGCCC ATCGTCAACC
TGAAGGACGA 240

GGTGCTATCT CCCAGCTGGG ACTCCCTGTT TTCTGGCTCC CAGGGTCAAC
TGCAACCCGG 300

GGCCCGCATC TTTTCTTTTG ACGGCAGAGA TGTCCTGAGA CACCCAGCCT
GGCCGCAGAA 360

GAGCGTATGG CACGGCTCGG ACCCCAGTGG GCGGAGGCTG ATGGAGAGTT
ACTGTGAGAC 420

ATGGCGAACT GAAACTACTG GGGCTACAGG TCAGGCCTCC TCCCTGCTGT
CAGGCAGGCT 480

CCTGGAACAG AAAGCTGCGA GCTGCCACAA CAGCTACATC GTCCTGTGCA
TTGAGAATAG 540

CTTCATGACC TCTTTCTCCA AATAG 565

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CTATCGTCGA CATGTATATT GGTTCCTCGTT AAGTCGACCT ATC

43

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GATAGGTCGA CTTAACGAGA ACCAATATAC ATGTCGACGA TAG

43

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGTATCTAGA ATGAGTGTAT CTGTCACAAT G

31

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GAATTCTAGA TCACCTATGA GGGGTTTGCT C

31

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CTATCGTCGA CATGTATATT GGTTCCTCGTA AAAGATATAT TGGTTCTCGT
GGTAAAAGAG 60

ATGGTTCTCG TGGTAAAAGA TAAGTGACCT ATC

93

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GATAGGTCGA CTTAT

15